

## SEQUENCE LISTING

<110> Hermon-Taylor, John  
 Doran, Tim  
 Millar, Douglas  
 Tizard, Mark  
 Loughlin, Mark  
 Sumar, Nazira

<120> NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC  
 MYCOBACTERIA AND THEIR USE AS DIAGNOSTICS, VACCINES AND  
 TARGETS FOR CHEMOTHERAPY

<130> 117-260

<140> 09/091,538

<141> 1998-06-19

<150> PCT/GB96/03221

<151> 1996-12-23

<150> GB 9526178.0

<151> 1995-12-21

<160> 41

<170> PatentIn Ver. 2.0

<210> 1

<211> 674

<212> DNA

<213> Mycobacterium

<400> 1

```

gatccaacta aacccgatgg aacccgcgc aaactattgg acgtctccgc gctacgcagt 60
tggtgtggcg cccgcgaatc gactgaaag agggcatcga tgcaacggtg tcgtgtgacc 120
gcacaaatgc cgatgccgtg aggaggtaaa gctgcggggc ggccgatgtt atccctccgg 180
ccggacgggt agggcgacct gccatcgagt ggtacggcag tcgcctggcc ggcgaggcgc 240
atggcctatg tgagtatccc atagcctggc ttggctcgcc cctacgcatt atcagttgac 300
cgcttttcgcg ccacgtcgca ggcttgccgc agcatcccg tccaggtctcc tcatggtccg 360
gtgtggcacg accacgcaag ctggaaccga ctcgtttccc aatttcgcat gctaataatcg 420
ctcgatggat tttttgcgca acgcccgtt gatggctcgt aacgttagca ccgagatgct 480
gcgccactcc gaacgaaagc gcctattagt aaaccaagtc gaagcatatg gactcaacgt 540
tggtattgat gtcggtgcta actccggcca gttcggtagc gctttgcgtc gtgcaggatt 600
caagagccgt atcgtttctt ttgaacctct ttcggggcca tttgcgcaac taacgcgcaa 660
gtcggcatcg gatc

```

674

<210> 2

<211> 674

<212> DNA

<213> Mycobacterium

<400> 2

```

gatccgatgc cgacttgccg gttagttgcg caaatggccc cgaaagaggt tcaaaggaaa 60
cgatacggct cttgaatcct gcacgacgca aagcgctacc gaactggccg gagttagcac 120
cgacatcaat aacaacgttg actccgtatg cttcgacttg gtttactaat aggcgctttc 180
gttcggagtg gcgcagcatc tcggtgctaa cgttacgagc catcaagccg gcgttgcgca 240
aaaaatccat cgagcgatat tagcatgcga aattgggaaa cgagtcgggt cgagcttgcg 300
tggtcgtgcc acaccggacc atgaggagac ctgaacggga tgctgccgca agcctgcgac 360
gtggcgcgaa agcgggtcaac tgataatgcg taggggagag ccaagccagg ctatgggata 420
ctcacatagg ccatgcgcct cgccggccag gcgactgccg taccactcga tggcaggtcg 480
ccctaccctg ccggccggag ggataacatc ggccggcccg cagctttacc tcctcacggc 540
atcggcattt gtgcggtacc acgacaccgt tgcacgatg ccctctttca gtgcgattcg 600
cgggcgccaa cccaactgcg tagcgcgag acgtccaata gtttgcgcg ggttccatcg 660
ggtttagttg gatc 674

```

<210> 3

<211> 7995

<212> DNA

<213> Mycobacterium

<400> 3

```

gaattctggg ttggagacga cgtcgaactc ctggtcggtc ttgcttcgaa tgatcgctgt 60
gatctggtcg gcggtgccga caggaaccgt cgacttgctg acgatcacct tgtaccggtc 120
gatgtatgac ccaatgtcgt ccgcaaccga gaagacgtac gtcagggtccg ccgccccgct 180
ttcaccatg ggctcgga cggcgatgaa aatgacgtcc gcgtgctcga ttccgcgttg 240
ccggtcggtg gtgaagtcaa tcagcccggt ctacgggttc ctgcgaatca actcccaacc 300
cgggctcgaa aatcgggaca ctgcctgcga ggagcaaata gatcttgacc tgatcgatat 360
cgacacagac gacatcggtg ccgctatccg cgagacaggc gcccgtagcg aggcctacat 420
agcctgatcc gaccaccgaa attttcaaga tgacccttc aagtccccga tcggtcgacg 480
accatactgc cgcaactctg taccctccgt gggtaattcg catgtcgcgt tcgtaaggag 540
cagccagcga gtcggggacg ttcggtgaga gagtcgagg actacgaggt tgccggtgcg 600
atacatcaca gtgttgctc tgtcggcaac gatgcagcaa gaaccacgg ggagccctg 660
aactgcgcgc atgaccggtc cttgtcctgg cacctttgat cggccaccgc ttccatgcga 720
acatgaccgg aatccatagc gcgtggtcaa gcagcgggga ggtagacgtc ggtgtcatct 780

```

gctccaaccg tgtcggatgat aacgatttcg ctgaacgatc tcgagggatt gaaaagcacc 840  
 gtggagagcg ttccgcgcga gcgctatggg gggcgaatcg agcacatcgt catcgacggg 900  
 ggatcggggcg acgccgtcgt ggagtatctg tccggcgatc ctggctttgc atattggcaa 960  
 tctcagccccg acaacgggag atatgacgcg atgaatcagg gcattgcccc ttcgtcgggc 1020  
 gacctgttgt ggtttatgca ctccacggat cgtttctccg atccagatgc agtcgcttcc 1080  
 gtggtggagg cgctctcggg gcatggacca gtacgtgatt tgtgggggta cgggaaaaac 1140  
 aaccttgtcg gactcgacgg caaaccactt ttccctcggc cgtacggcta tatgccgttt 1200  
 aagatgcgga aatttctgct cggcgcgacg gttgcgcac caggcgacatt cttcggcgcg 1260  
 tcgctggtag ccaagttggg cggttacgat cttgattttg gactcgaggc ggaccagctg 1320  
 ttcacttacc gtgccgcact aatacggcct cccgtcacga tcgaccgcgt ggtttgcgac 1380  
 ttcgatgtca cgggacctgg ttcaaccag cccatccgtg agcactatcg gacctgcgg 1440  
 cggctctggg acctgcatgg cgactaccgg ctgggtgggc gcagagtgtc gtgggcttac 1500  
 ttgcgtgtga aggagtactt gattcggggc gacctggccg cattcaacgc ggtaaagtcc 1560  
 ttgcgagcga agttcgccag agcttcgcgg aagcaaaatt catagaaacc aacttctact 1620  
 gcctgacctg agcagcgccg aggcgcgcag cgcgatcagt gcgacctgaa cggccaggtg 1680  
 gaaagcgcca ccgatcccg caccgagtgc ctgacgcttc ggatcccttg caccacaacg 1740  
 agagtgagag cgccatgatg aggaaatata ggctgggcgg agtcaacgcc ggagtgacaa 1800  
 aagtgagaac ccggtgaagc gagcgcttat aacagggatc acggggcagg atggttcccta 1860  
 cctcgccgag ctactactga gcaagggata cgaggttcac gggctcgttc gtcgagcttc 1920  
 gacgtttaac acgtcgcgga tcgatcacct ctacgttgac ccacaccaac cgggcgcgcg 1980  
 cttgttcttg cactatgcag acctcactga cggcaccggg ttggtgacct tgctcagcag 2040  
 tatcgaccgg gatgaggtct acaacctcgc agcgcagtc ccatgtgcgcg tcagctttga 2100  
 cgagccagtg cataccggag acaccaccgg catgggatcg atccgacttc tggaagcagt 2160  
 ccgcctttct cgggtggact gccggttcta tcaggcttcc tcgtcggaga tgttcggcgc 2220  
 atctccgcca ccgcagaacg aatcgacgcc gttctatccc cgttcgccat acggcgcggc 2280  
 caaggtcttc tcgtactgga cgactcgcaa ctatcgagag gcgtacggat tattcgcagt 2340  
 gaatggcatc ttgttcaacc atgagtcccc cgggcgcggc gagactttcg tgacccgaaa 2400  
 gatcacgcgt gccgtggcgc gcatccgagc tggcggtccaa tcggaggtct atatgggcaa 2460  
 cctcgatgcg atccgcgact ggggctacgc gccgaatat gtcgagggga tgtggaggat 2520  
 gttgcaagcg cctgaacctg atgactacgt cctggcgaca gggcgtggtt acaccgtacg 2580  
 tgagttcgct caagctgctt ttgacctgt cgggctcgac tggcaaaagc gcgtcaagtt 2640

tgacgaccgc tatttgctc ccaccgaggt cgattcgcta gtaggagatg ccgacaaggc 2700  
ggcccagtc ctcggctgga aagcttcggt tcatactggt gaactcgcg gcacatcggt 2760  
ggacgcggac atcgccgct tggagtgcga tggcacacca tggatcgaca cgccgatgtt 2820  
gcttggttg ggcagagtaa gttgacgact acacctgggc ctctggaccg cgcaacgccc 2880  
gtgtatatcg ccggtcatcg ggggctggtc ggctcagcgc tcgtacgtag atttgaggcc 2940  
gaggggttca ccaatctcat tgtgcgatca cgcgatgaga ttgatctgac ggaccgagcc 3000  
gcaacgtttg attttgtgtc tgagacaaga ccacaggtga tcatcgatgc ggccgcacgg 3060  
gtcggcggca tcatggcgaa taacacctat ccgcgggact tcttgtccga aaacctccga 3120  
atccagacca atttgctcga cgcagctgtc gccgtgctg tgccgcggct ccttttctc 3180  
ggttcgtcat gcacctacc gaagtacgct ccgcaaccta tccacgagag tgctttattg 3240  
actggccctt tggagccac caacgacgcg tatgcgatcg ccaagatcgc cgtatcctg 3300  
caagttcagg cggttaggcg ccaatatggg ctggcgtgga tctctgcgat gccgactaac 3360  
ctctacggac ccggcgacaa cttctccccg tccgggtcgc atctcttgcc ggcgctcctc 3420  
cgtcgatatg aggaagccaa agctggtggt gcagaagagg tgacgaattg ggggaccggt 3480  
actccgcggc gcgaacttct gcacgtcgc gatctggcga gcgcacgcct gttcctttt 3540  
gaacatttcg atggtccgaa ccacgtcaac gtgggcaccg gcgtcgatca cagcattagc 3600  
gagatcgag acatggctgc tacagcgggt ggctacatcg gcgaaacacg ttgggatcca 3660  
actaaacccg atggaacccc gcgcaaacta ttggacgtct ccgcgctacg cgagttgggt 3720  
tggcgccgc gaatcgact gaaagacggc atcgatgcaa cgggtgctgt gtaccgcaca 3780  
aatgccgatg ccgtgaggag gtaaagctgc gggtcggccg atgttatccc tccggccgga 3840  
cgggtggggc gacctgccgt cgagtggtag ggacgtcgcc tggccggcga ggcgctggc 3900  
ctatgggagt atccaatagc ctggcttggc tgcacctac gcattatcag ttgaccgctt 3960  
tcgcgccagc tcgcaggctt gcggcagcat ccggttcagg tctcctcatg gtccggtgtg 4020  
gcacgaccac gcaagctcga accgactcgt ttcccaattt cgcacgctaa tatcgctcga 4080  
tggatttttt gcgcaacgcc ggcttgatgg ctcgtaacgt tagtaccgag atgctgcgcc 4140  
acttcgaacg aaagcgcta ttagtaaac aattcaaagc atacggagtc aacgttgta 4200  
ttgatgtcgg tgctaactcc ggccagttcg gtagcgcttt gcgtcgtgca ggattcaaga 4260  
gccgtatcgt ttcttttgaa cctctttcgg ggccatttgc gcaactaacg cgcaagtcgg 4320  
catcggatcc actatgggag tgtcaccagt atgcctagg cgacgccgat gagacgatta 4380  
ccatcaatgt ggcaggcaat gcgggggcaa gtagttccgt gctgccgatg cttaaaagtc 4440

atcaagatgc ctttctctcc gcgaattata ttggcaccga agacgttgca atacaccgcc 4500  
 ttgattcgggt tgcatacagaa tttctgaacc ctaccgatgt tactttctctg aagatcgacg 4560  
 tacaggggttt cgagaagcag gttatcacgg gcagtaagtc aacgcttaac gaaagctgcg 4620  
 tcggcatgca actcgaactt tcttttatte cgttgtacga aggtgacatg ctgattcatg 4680  
 aagcgcttga acttgtctat tccctagggt tcagactgac gggtttggtg cccggcttta 4740  
 cggatccgcg caatggtcga atgcttcaag ctgacggcat tttcttccgt ggggacgatt 4800  
 gacataaatg ctccgtcggc accctgccgg tatccaaacg ggcgatctgg tgagccggcc 4860  
 tcccgggcac ctaatcgact atctaaattg aggcgccgc gacgtgcggc acgaacaggt 4920  
 ggccggctgc tagcggtaca cacgtcatga ctgcgccagt gttctcgata attatcccta 4980  
 ccttcaatgc agcggtgacg ctgcaagcct gcctcggaag catcgtcggg cagacctacc 5040  
 gggaagtgga agtggtcctt gtcgacggcg gttcgaccga tcggaccctc gacatcgca 5100  
 acagtttccg cccggaactc ggctcgcgac tggtcgttca cagcggggcc gatgatggcc 5160  
 cctacgacgc catgaaccgc ggctcggcg tggccacagg cgaatgggta ctttttttag 5220  
 gcgccgacga caccctctac gaaccaacca cgttggccca ggtagccgct tttctcggcg 5280  
 accatgcggc aagccatctt gtctatggcg atgttgtgat gcgttcgacg aaaagccggc 5340  
 atgccggacc tttcgacctc gaccgcctcc tatttgagac gaatttgtgc caccaatcga 5400  
 tcttttaccg ccgtgagctt ttcgacggca tcggccctta caacctgcgc taccgagtct 5460  
 gggcggaactg ggacttcaat attcgtgct tctccaacc ggcgctgatt acccgctaca 5520  
 tggacgtcgt gatttccgaa tacaacgaca tgaccggctt cagcatgagg caggggactg 5580  
 ataaagagtt cagaaaacgg ctgccaatgt acttctgggt tgcagggtgg gagacttgca 5640  
 ggcgcatgct ggcgtttttg aaagacaagg agaatcgccg tctggccttg cgtacgcgg 5700  
 tgataaggggt taaggccgtc tccaaagaac gaagcgcaga accgtagtcg cggatccaca 5760  
 ttggacttct ttaacgcgtt tgcgtcctga tccaccttc aagcccgttc cgcgtaacgc 5820  
 ggcgcgacga gagtggctgc atatcgcatc actgttctcg tgccagtgct tggaaagcgt 5880  
 cgagcactct ggttcgcgtt cttgacgttc gcgcccgtc ctagaggtag cgtgtcacgt 5940  
 gactgaagcc aatgagtga actcggcgtc gcgaaagggt tcagtcgcgg ttgagcaaga 6000  
 caccgcaaga ctactggagt gcgtgcacaa gcgcctccag ctgcggctg aaagcggatg 6060  
 caaagggatt cgaagcttga gcaacatgcg aaggggagaa cggcctatga ggctgggaca 6120  
 ggttttcgat ccgcgcgca atgcactgtc aatggccaag tagaagtccc cgctggtggc 6180  
 cagcagaagt cccactccg ctgcgggtgg ttggctaatt cttggcggct cccttcttgt 6240  
 ggtcggcgtg gcgcatccgg taggactcgc cggagggtgac gacgatgctg gcgtggtgca 6300

gcagccgatac gaggatgctg gcggcggtgg tgtgctcggg caggaatcgc cccattgtt 6360  
cgaagggcca atgcgaggcg atggccaggg agcggcgctc gtagccggca gccacgagcc 6420  
ggaacaacag ttgagtcccg gtgtcgtcga gcggggcgaa gccgatctcg tccaagatga 6480  
ccagatccgc gcggagcagg gtgtcgtatga tcttgccgac ggtgttgctg gccaggccgc 6540  
ggtagaggac ctcgatcagg tcggcgggcg tgaagtagcg gactttgaat ccggcgtgga 6600  
cggcagcgtg cccgcagccg atgagcaggt gacttttgcc cgtaccaggt gggccaatga 6660  
ccgccagggt ctgttggtgc cgaatccatt ccaggctcga caggtagtcg aacgtggctg 6720  
cggtgatcga cgatccggtg acgtcgaacc cgtcgagggt cttggtgacc gggaaggctg 6780  
cggccttgag acggttggtg gtgttgagg catcggggc agcgatctcg gcctcaacca 6840  
acgtccgcag gatctcctcc ggtgtccagc gttgcgtctt ggcgacttgc aacacctcgg 6900  
cggcgttgcg gcgcaccgtg gccagcttca accgccgcag cgcgcgtca aggtcagcag 6960  
ccagcgggtc cgcgaggac ggtgccaccg gcttggcagc ggtggtcatt aggccgtccc 7020  
gtcggtggtg ttgatcttgt aggcctccaa cgagcgggtc tcgacgggtg gcagatcgag 7080  
cacgagtgcg tcgccggcg ggccggggtt tggggtgccg gcgccggcg ccaggatcga 7140  
gcgcacgtcg gcagcgcgga accggcgaaa cgcaaccgcc cggcgcagcg cgtcaatcaa 7200  
agcctgttcg ccgtgggcgg cgccaaggcc gagcagaatg tcgagttcgg atttcagtcg 7260  
ggtgttgccg atcgcagcag caccgacgag gaactgctgc gcttcgggtc ccaatgcgca 7320  
gaatcgtttc tctgcttggg ttttcgggcg aggaccacgc gagggtgcgg gtctgggtcc 7380  
gtcgtagtgt tcatcgagga tggacacctc acctgggctg acgagctcgt gtcgggccac 7440  
gatcacaccg gtcgcaggtt ccaacaggat cagggcgcca tgatcgacca ccaccgccac 7500  
ggtggcaccg acgagccgct gaggcaccga gtaacgagct gagccgtaac ggatgcacga 7560  
gaggccgtcg acctacggc gcaccgacct cgagccgata gtcggccgca gcgagggcag 7620  
ctccctcaag acggtgcgt cgtcaaccaa gcgatcgttg ggcacggcgc agatctccga 7680  
gtggaccgtg gcattgacct cggcgcacca tagttgcgcc tgggcgttga gggcacgtag 7740  
gtcgacctgc tcaccggcta acgcagcttc ggtcagcagc ggcaccgcaa ggtcgtcctg 7800  
agcgtagcca cagagttct ccacgatgcc cttegatctg ggatccgcac cgtggcagaa 7860  
gtccggaacg aagccatagt gggacgcgaa tcgcacataa tccggtgttg gaacaacaac 7920  
attggcgacg acaccacctt tgaggcagcc catccggctg gccaggatct tggccggaac 7980  
cccaccgata gcctc 7995

<211> 4435  
 <212> DNA  
 <213> Mycobacterium

<400> 4

```

ttctactgcc tgacctgagc agcgccgagg cgcgccagcgc gatcactgcg acctgaatgg 60
ccagggtggaa agcgccaccg atcccgccac cgagtgcctg acgattcgga tcccttgccac 120
cacaacgaga gtgagaccgc catgatgacg aaatatcggc tgggcggagt caacgccgga 180
gtgacaaaaag tgagaacccg gtgaagcgag cgcttataac agggatcacg gggcaggatg 240
gttctctacct cgccgagcta ctactgagca agggatacga ggttcacggg ctcgttcgtc 300
gagcttcgac gtttaacacg tcgcggatcg atcacctcta cgttgaccca caccaaccgg 360
gcgcgcgctt gttcttgac tatgcagacc tcaactgacgg caccgcggtg gtgaccctgc 420
tcagcagtat cgaccggat gaggtctaca acctcgcagc gcagtcccat gtgcgcgtca 480
gctttgacga gccagtgcac accggagaca ccaccggcat gggatcgatc cgacttctgg 540
aagcagtccg cttttctcgg gtggactgcc ggttctatca ggcttcctcg tcggagatgt 600
tcggcgcacg tccgccaccg cagaacgaat cgacgcgctt ctatccccgt tcgccatacg 660
gcgcggccaa ggtcttctcg tactggacga ctgcgaacta tcgagaggcg tacggattat 720
tcgcagtgaa tggcatcttg ttcaaccatg agtccccccg gcgcggcgag actttcgtga 780
cccgaagat cacgcgtgcc gtggcgcgca tccgagctgg ctgccaatcg gaggtctata 840
tgggcaacct cgatgcgacg cgcgactggg gctacgcgcc cgaatatgtc gaggggatgt 900
ggaggatggt gcaagcgctt gaacctgatg actacgtcct ggcgacaggg cgtgggttaca 960
ccgtacgtga gttcgctcaa gctgcttttg accacgtcgg gctcgactgg caaaagcacg 1020
tcaagtttga cgaccgctat ttgcgcccc cagaggctga ttcgctagta ggagatgccg 1080
acagggcggc ccagtcactc ggctggaaag cttcgggttca tactggtgaa ctgcgcgcga 1140
tcatggtgga cgcgacacg gccgcgtcgg agtgcgatgg cacaccatgg atcgacacgc 1200
cgatggtgcc tgggtggggc ggagtaagtt gacgactaca cctgggcctc tggaccgcgc 1260
aacgcccgtg tatatcgccg gtcacgggg gctggtcggc tcagcgctcg tacgtagatt 1320
tgaggccgag gggttcacca atctcattgt gcgatcacgc gatgagattg atctgacgga 1380
ccgagccgca acgtttgatt ttgtgtctga gacaagacca caggtgatca tcgatgcggc 1440
cgcacgggtc ggcgccatca tggcgaataa cacctatccc gcggacttct tgtccgaaaa 1500
cctccgaatc cagaccaatt tgctcgacgc agctgtcgcc gtgcgtgtgc cgcggtcct 1560
tttctcgggt tcgtcatgca tctacccgaa gtacgctccg caacctatcc acgagagtgc 1620
tttattgact ggccctttgg agcccaccaa cgacgcgtat gcgatcgcca agatcgccgg 1680

```

tatcctgcaa gttcaggcgg ttaggcgcca atatgggctg gcgtggatct ctgcgatgcc 1740  
gactaacctc tacggacccg gcgacaactt ctccccgtcc gggtcgcac ctttgccggc 1800  
gctcatccgt cgatatgagg aagccaaagc tgggtggtgca gaagaggtga cgaattgggg 1860  
gaccggtact ccgcggcgcg aacttctgca tgtcgacgat ctggcgagcg catgcctgtt 1920  
ccttttggaa catttcgatg gtccgaacca cgtcaacgtg ggcaccggcg tcgatcacag 1980  
cattagcgag atcgagaca tggtcgctac ggcggtgggc tacatcggcg aaacacgttg 2040  
ggatccaact aaaccgatg gaaccggcg caaactattg gacgtctccg cgctacgca 2100  
gttgggttg cgcccgcaa tcgcactgaa agacggcatc gatgcaacgg tgcgtggta 2160  
ccgcacaaat gccgatgccg tgaggaggta aagctgcggg ccggccgatg ttatccctcc 2220  
ggccggacgg gtagggcgac ctgccatcga gtggtacggc agtcgcctgg ccggcgaggc 2280  
gcatggccta tgggagtatc ccatagcctg gcttggctcg cccctacgca ttatcagttg 2340  
accgctttcg cgccagctcg caggctcgcg gcagcatccc gttcaggtct cctcatggtc 2400  
cggtgtggca cgaccacgca agctcgaacc gactcgtttc ccaatttcgc atgctaatat 2460  
cgctcgatgg attttttgcg caacgcggc ttgatggctc gtaacgtag caccgagatg 2520  
ctgcgccact tcgaacgaaa gcgcctatta gtaaaccaat tcaaagcata cggagtcaac 2580  
gttggtattg atgtcgggtc taactccggc cagttcggtg gcgctttgcg tcgtgcagga 2640  
ttcaagagcc gtatcgtttc ctttgaacct ctttcggggc catttgcgca actaacgcgc 2700  
gagtcggcat cggatccact atgggagtgt caccagtatg ccctaggcga cgccgatgag 2760  
acgattacca tcaatgtggc aggcaatgcg ggggcaagta gttccgtgct gccgatgctt 2820  
aaaagtcac aagatgcctt tcctcccgcg aattatattg gcaccgaaga cgttgcaata 2880  
caccgccttg attcggttgc atcagaattt ctgaacccta ccgatgttac tttcctgaag 2940  
atcgacgtac agggtttcga gaagcagggt atcgcgggca gtaagtcaac gcttaacgaa 3000  
agctgcgtcg gcatgcaact cgaactttct tttattccgt tgtacgaagg tgacatgctg 3060  
attcatgaag cgcttgaact tgtctattcc ctaggtttca gactgacggg tttgttggcc 3120  
ggatttacgg atccgcgcaa tggtcgaatg cttcaagctg acggcatttt cttccgtggg 3180  
gacgattgac ataaatgctt gcgtcggcac cctgccggta tccaaacggg cgatctggtg 3240  
agccggcctc ccgggcacct aatcgactat ctaaattgag gcggcccgca cgtgcggcac 3300  
gaacagggtg ccggctgcta gcgttacaca cgtcatgact gcgccagtgt tctcgataat 3360  
tatccctacc ttcaatgcag cggtgacgt gcaagcctgc ctcggaagca tcgtcgggca 3420  
gacctaccgg gaagtgaag tggtccttgt cgacggcggg tcgaccgatc ggaccctcga 3480  
catcgcgaa agtttccgcc cggaactcgg ctcgcgactg gtcgttcaca gcgggcccga 3540



tgatggcccc tacgacgcca tgaaccgagg cgtcggcgta gccacaggcg aatgggtact 3600  
 ttttttaggc gccgacgaca ccctctacga accaaccacg ttggcccagg tagccgcttt 3660  
 tctcggcgac catgcgga gcatcttgt ctatggcgat gttgtgatgc gttcgacgaa 3720  
 aagccggcat gccggacctt tcgacctga ccgcctccta tttgagacga atttgtgcca 3780  
 ccaatcgatc ttttaccgcc gtgagctttt cgacggcacc ggcccttaca acctgcgcta 3840  
 ccgagtctgg gcggactggg acttcaatat tcgctgcttc tccaacccgg cgctgattac 3900  
 ccgctacatg gacgtcgtga tttccgaata caacgacatg accggttca gcatgaggca 3960  
 ggggactgat aaagagttca gaaaacggct gccaatgtac ttctgggttg caggggtgga 4020  
 gacttgacagg cgcatgctgg cgtttttgaa agacaaggag aatcgccgtc tggccttgcg 4080  
 tacgcggttg ataagggtta aggccgtctc caaagaacga agcgacagac cgtagtcgag 4140  
 gatccacatt ggacttcttt aacgcgtttg cgctctgac cacttttcaa ccccgttccg 4200  
 cgtgacgcgg cgcgacgaga gtggtcgcat atcgcgctac tgttctcgtg ccagtgcctg 4260  
 gaaagcgctg agcactctgg ttcgcgttct tgacgttcgc gcccggccct agaggtagcg 4320  
 tgtcacgtga ctgaagccaa tgagtgaac tcggcgctgc gaaaggtttc agtcgcgggt 4380  
 gagcaagaca ccgcaagact actggagtgc gtgcacaagc gcctccagct cacgg 4435

<210> 5

<211> 378

<212> DNA

<213> Mycobacterium

<220>

<221> CDS

<222> (1)..(375)

<400> 5

atg atc gct gtg atc tgg tgc gcg gtg ccg aca gga acc gtc gac ttg	48
Met Ile Ala Val Ile Trp Ser Ala Val Pro Thr Gly Thr Val Asp Leu	
1 5 10 15	
tcg acg atc acc ttg tac cgg tgc atg tat gac cca atg tgc tcc gca	96
Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala	
20 25 30	
acc gag aag acg tac gtc agg tcc gcc gcc ccg ctt tca ccc atg ggc	144
Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly	
35 40 45	
gtc ggg acg gcg atg aaa atg acg tcc gcg tgc tgc att ccg cgt tgc	192
Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys	
50 55 60	
cgg tgc gtg gtg aag tca atc agc ccg ttc tca cgg ttc ctc gca atc	240
Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile	
65 70 75 80	



ctc gag gga ttg aaa agc acc gtg gag agc gtt cgc gcg cag cgc tat	96
Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr	
20 25 30	
ggg ggg cga atc gag cac atc gtc atc gac ggt gga tcg ggc gac gcc	144
Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala	
35 40 45	
gtc gtg gag tat ctg tcc ggc gat cct ggc ttt gca tat tgg caa tct	192
Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser	
50 55 60	
cag ccc gac aac ggg aga tat gac gcg atg aat cag ggc att gcc cat	240
Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His	
65 70 75 80	
tcg tcg ggc gac ctg ttg tgg ttt atg cac tcc acg gat cgt ttc tcc	288
Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser	
85 90 95	
gat cca gat gca gtc gct tcc gtg gtg gag gcg ctc tcg ggg cat gga	336
Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly	
100 105 110	
cca gta cgt gat ttg tgg ggt tac ggg aaa aac aac ctt gtc gga ctc	384
Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu	
115 120 125	
gac ggc aaa cca ctt ttc cct cgg ccg tac ggc tat atg ccg ttt aag	432
Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys	
130 135 140	
atg cgg aaa ttt ctg ctc ggc gcg acg gtt gcg cat cag gcg aca ttc	480
Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe	
145 150 155 160	
ttc ggc gcg tcg ctg gta gcc aag ttg ggc ggt tac gat ctt gat ttt	528
Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe	
165 170 175	
gga ctc gag gcg gac cag ctg ttc atc tac cgt gcc gca cta ata cgg	576
Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg	
180 185 190	
cct ccc gtc acg atc gac cgc gtg gtt tgc gac ttc gat gtc acg gga	624
Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly	
195 200 205	
cct ggt tca acc cag ccc atc cgt gag cac tat cgg acc ctg cgg cgg	672
Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg	
210 215 220	
ctc tgg gac ctg cat ggc gac tac ccg ctg ggt ggg cgc aga gtg tcg	720
Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser	
225 230 235 240	
tgg gct tac ttg cgt gtg aag gag tac ttg att cgg gcc gac ctg gcc	768
Trp Ala Tyr Leu Arg Val Lys Glu Tyr Leu Ile Arg Ala Asp Leu Ala	
245 250 255	

816

834

<400> 8															
Val	Ser	Ser	Ala	Pro	Thr	Val	Ser	Val	Ile	Thr	Ile	Ser	Leu	Asn	Asp
1				5					10					15	
Leu	Glu	Gly	Leu	Lys	Ser	Thr	Val	Glu	Ser	Val	Arg	Ala	Gln	Arg	Tyr
			20					25					30		
Gly	Gly	Arg	Ile	Glu	His	Ile	Val	Ile	Asp	Gly	Gly	Ser	Gly	Asp	Ala
		35					40					45			
Val	Val	Glu	Tyr	Leu	Ser	Gly	Asp	Pro	Gly	Phe	Ala	Tyr	Trp	Gln	Ser
	50					55					60				
Gln	Pro	Asp	Asn	Gly	Arg	Tyr	Asp	Ala	Met	Asn	Gln	Gly	Ile	Ala	His
65					70					75					80
Ser	Ser	Gly	Asp	Leu	Leu	Trp	Phe	Met	His	Ser	Thr	Asp	Arg	Phe	Ser
				85					90					95	
Asp	Pro	Asp	Ala	Val	Ala	Ser	Val	Val	Glu	Ala	Leu	Ser	Gly	His	Gly
			100					105					110		
Pro	Val	Arg	Asp	Leu	Trp	Gly	Tyr	Gly	Lys	Asn	Asn	Leu	Val	Gly	Leu
		115					120					125			
Asp	Gly	Lys	Pro	Leu	Phe	Pro	Arg	Pro	Tyr	Gly	Tyr	Met	Pro	Phe	Lys
	130					135					140				
Met	Arg	Lys	Phe	Leu	Leu	Gly	Ala	Thr	Val	Ala	His	Gln	Ala	Thr	Phe
145					150					155					160
Phe	Gly	Ala	Ser	Leu	Val	Ala	Lys	Leu	Gly	Gly	Tyr	Asp	Leu	Asp	Phe
				165					170					175	
Gly	Leu	Glu	Ala	Asp	Gln	Leu	Phe	Ile	Tyr	Arg	Ala	Ala	Leu	Ile	Arg
			180					185					190		
Pro	Pro	Val	Thr	Ile	Asp	Arg	Val	Val	Cys	Asp	Phe	Asp	Val	Thr	Gly
		195					200					205			
Pro	Gly	Ser	Thr	Gln	Pro	Ile	Arg	Glu	His	Tyr	Arg	Thr	Leu	Arg	Arg
	210					215					220				
Leu	Trp	Asp	Leu	His	Gly	Asp	Tyr	Pro	Leu	Gly	Gly	Arg	Arg	Val	Ser
225					230					235					240

<400>																
gtg	aag	cga	gcg	ctt	ata	aca	ggg	atc	acg	ggg	cag	gat	ggg	tcc	tac	48
Val	Lys	Arg	Ala	Leu	Ile	Thr	Gly	Ile	Thr	Gly	Gln	Asp	Gly	Ser	Tyr	
1				5				10						15		
<hr/>																
ctc	gcc	gag	cta	cta	ctg	agc	aag	gga	tac	gag	gtt	cac	ggg	ctc	gtt	96
Leu	Ala	Glu	Leu	Leu	Leu	Ser	Lys	Gly	Tyr	Glu	Val	His	Gly	Leu	Val	
			20				25						30			
<hr/>																
cgt	cga	gct	tcg	acg	ttt	aac	acg	tcg	cgg	atc	gat	cac	ctc	tac	gtt	144
Arg	Arg	Ala	Ser	Thr	Phe	Asn	Thr	Ser	Arg	Ile	Asp	His	Leu	Tyr	Val	
			35				40						45			
<hr/>																
gac	cca	cac	caa	ccg	ggc	gcg	cgc	ttg	ttc	ttg	cac	tat	gca	gac	ctc	192
Asp	Pro	His	Gln	Pro	Gly	Ala	Arg	Leu	Phe	Leu	His	Tyr	Ala	Asp	Leu	
50					55						60					
<hr/>																
act	gac	ggc	acc	cgg	ttg	gtg	acc	ctg	ctc	agc	agt	atc	gac	ccg	gat	240
Thr	Asp	Gly	Thr	Arg	Leu	Val	Thr	Leu	Leu	Ser	Ser	Ile	Asp	Pro	Asp	
65					70						75			80		
<hr/>																
gag	gtc	tac	aac	ctc	gca	gcg	cag	tcc	cat	gtg	cgc	gtc	agc	ttt	gac	288
Glu	Val	Tyr	Asn	Leu	Ala	Ala	Gln	Ser	His	Val	Arg	Val	Ser	Phe	Asp	
				85				90						95		
<hr/>																
gag	cca	gtg	cat	acc	gga	gac	acc	acc	ggc	atg	gga	tcg	atc	cga	ctt	336
Glu	Pro	Val	His	Thr	Gly	Asp	Thr	Thr	Gly	Met	Gly	Ser	Ile	Arg	Leu	
			100				105						110			
<hr/>																
ctg	gaa	gca	gtc	cgc	ctt	tct	cgg	gtg	gac	tgc	cgg	ttc	tat	cag	gct	384
Leu	Glu	Ala	Val	Arg	Leu	Ser	Arg	Val	Asp	Cys	Arg	Phe	Tyr	Gln	Ala	
			115				120						125			
<hr/>																
tcc	tcg	tcg	gag	atg	ttc	ggc	gca	tct	ccg	cca	ccg	cag	aac	gaa	tcg	432
Ser	Ser	Ser	Glu	Met	Phe	Gly	Ala	Ser	Pro	Pro	Pro	Gln	Asn	Glu	Ser	
130					135						140					
<hr/>																
acg	ccg	ttc	tat	ccc	cgt	tcg	cca	tac	ggc	gcg	gcc	aag	gtc	ttc	tcg	480
Thr	Pro	Phe	Tyr	Pro	Arg	Ser	Pro	Tyr	Gly	Ala	Ala	Lys	Val	Phe	Ser	
145					150						155			160		

tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg	528
Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val	
165 170 175	
aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc	576
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe	
180 185 190	
gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc	624
Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val	
195 200 205	
caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc	672
Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly	
210 215 220	
tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct	720
Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro	
225 230 235 240	
gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt	768
Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg	
245 250 255	
gag ttc gct caa gct gct ttt gac cat gtc ggg ctc gac tgg caa aag	816
Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys	
260 265 270	
cgc gtc aag ttt gac gac cgc tat ttg cgt ccc acc gag gtc gat tcg	864
Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser	
275 280 285	
cta gta gga gat gcc gac aag gcg gcc cag tca ctc ggc tgg aaa gct	912
Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala	
290 295 300	
tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc	960
Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile	
305 310 315 320	
gcc gcg ttg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg	1008
Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu	
325 330 335	
cct ggt tgg ggc aga gta agt tga	1032
Pro Gly Trp Gly Arg Val Ser	
340	

&lt;210&gt; 10

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 10

Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
1 5 10 15

Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
20 25 30

Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
 325 330 335  
 Pro Gly Trp Gly Arg Val Ser  
 340

<210> 11  
 <211> 1032  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1029)

<400> 11  
 gtg aag cga gcg ctt ata aca ggg atc acg ggg cag gat ggt tcc tac 48  
 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr  
 1 5 10 15  
 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96  
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val  
 20 25 30  
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144  
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg 528  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc 576  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc 624  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205



caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc 672  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct 720  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt 768  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 gag ttc gct caa gct gct ttt gac cac gtc ggg ctc gac tgg caa aag 816  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 cac gtc aag ttt gac gac cgc tat ttg cgc ccc acc gag gtc gat tcg 864  
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 cta gta gga gat gcc gac agg gcg gcc cag tca ctc ggc tgg aaa gct 912  
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc 960  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 gcc gcg tcg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg 1008  
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
 325 330 335  
 cct ggt tgg ggc gga gta agt tga 1032  
 Pro Gly Trp Gly Gly Val Ser  
 340

&lt;210&gt; 12

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 12

Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr  
 1 5 10 15  
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val  
 20 25 30  
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95

Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
 325 330 335  
 Pro Gly Trp Gly Gly Val Ser  
 340

<210> 13  
 <211> 1020  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1017)

&lt;400&gt; 13

gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg	48
Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly	
1 5 10 15	
cag agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc	96
Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro	
20 25 30	
gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt	144
Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg	
35 40 45	
aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	

gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat 768  
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp  
 245 250 255  
 ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc 816  
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser  
 260 265 270  
 gag atc gca gac atg gtc gct aca gcg gtg ggc tac atc ggc gaa aca 864  
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr  
 275 280 285  
 cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300  
 gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320  
 gac ggc atc gat gca acg gtg tcg tgg tac cgc aca aat gcc gat gcc 1008  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335  
 gtg agg agg taa 1020  
 Val Arg Arg

<210> 14  
 <211> 339  
 <212> PRT  
 <213> Mycobacterium

<400> 14  
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly  
 1 5 10 15  
 Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro  
 20 25 30  
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg  
 35 40 45  
 Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp  
 50 55 60  
 Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu  
 65 70 75 80  
 Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile  
 85 90 95  
 Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg  
 100 105 110  
 Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg  
 115 120 125  
 Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln  
 130 135 140

Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn  
 145 150 155 160  
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala  
 165 170 175  
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn  
 180 185 190  
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu  
 195 200 205  
 Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu  
 210 215 220  
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His  
 225 230 235 240  
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp  
 245 250 255  
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser  
 260 265 270  
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr  
 275 280 285  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335  
 Val Arg Arg

<210> 15  
 <211> 1020  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1017)

<400> 15  
 gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg 48  
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly  
 1 5 10 15  
 cgg agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc 96  
 Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro  
 20 25 30  
 gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt 144  
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg  
 35 40 45

aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	
gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat	768
Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp	
245 250 255	
ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc	816
Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser	
260 265 270	
gag atc gca gac atg gtc gct acg gcg gtg ggc tac atc ggc gaa aca	864
Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr	
275 280 285	

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300  
  
 gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320  
  
 gac ggc atc gat gca acg gtg tcg tgg tac cgc aca aat gcc gat gcc 1008  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335  
  
 gtg agg agg taa 1020  
 Val Arg Arg

<210> 16  
 <211> 339  
 <212> PRT  
 <213> Mycobacterium

<400> 16  
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly  
 1 5 10 15  
  
 Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro  
 20 25 30  
  
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg  
 35 40 45  
  
 Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp  
 50 55 60  
  
 Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu  
 65 70 75 80  
  
 Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile  
 85 90 95  
  
 Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg  
 100 105 110  
  
 Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg  
 115 120 125  
  
 Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln  
 130 135 140  
  
 Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn  
 145 150 155 160  
  
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala  
 165 170 175  
  
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn  
 180 185 190  
  
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu  
 195 200 205

Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu  
 210 215 220

Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His  
 225 230 235 240

Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp  
 245 250 255

Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser  
 260 265 270

Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr  
 275 280 285

Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300

Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320

Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335

Val Arg Arg

<210> 17  
 <211> 723  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(720)

<400> 17  
 atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agt acc 48  
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
 1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96  
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
 20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144  
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
 35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192  
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
 50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc aag tcg 240  
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser  
 65 70 75 80

gca tcg gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288  
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
 85 90 95



gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt	336
Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser	
100 105 110	
tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg	384
Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala	
115 120 125	
aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt	432
Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val	
130 135 140	
gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac	480
Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp	
145 150 155 160	
gta cag ggt ttc gag aag cag gtt atc acg ggc agt aag tca acg ctt	528
Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu	
165 170 175	
aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg	576
Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu	
180 185 190	
tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc	624
Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser	
195 200 205	
cta ggt ttc aga ctg acg ggt ttg ttg ccc ggc ttt acg gat ccg cgc	672
Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg	
210 215 220	
aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat	720
Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp	
225 230 235 240	
tga	723

&lt;210&gt; 18

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 18

Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
1 5 10 15

Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
20 25 30

Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
35 40 45

Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
50 55 60

Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser
65 70 75 80

Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
85 90 95

Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
100 105 110

Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
115 120 125

Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
130 135 140

Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
145 150 155 160

Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu  
165 170 175

Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
180 185 190

Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
195 200 205

Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
210 215 220

Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
225 230 235 240

&lt;210&gt; 19

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Mycobacterium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(720)

&lt;400&gt; 19

atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agc acc 48  
Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96  
Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144  
Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192  
Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc gag tcg 240  
Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser  
65 70 75 80

gca tcg gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288  
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
                     85                    90                    95

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336  
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
                     100                    105                    110

tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384  
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
                     115                    120                    125

aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt 432  
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
                     130                    135                    140

gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480  
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
                     145                    150                    155                    160

gta cag ggt ttc gag aag cag gtt atc gcg ggc agt aag tca acg ctt 528  
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu  
                     165                    170                    175

aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576  
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
                     180                    185                    190

tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624  
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
                     195                    200                    205

cta ggt ttc aga ctg acg ggt ttg ttg ccc gga ttt acg gat ccg cgc 672  
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
                     210                    215                    220

aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720  
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
                     225                    230                    235                    240

tga 723

&lt;210&gt; 20

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 20

Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
           1                    5                    10                    15

Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
                     20                    25                    30

Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
                     35                    40                    45

Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
                     50                    55                    60

Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser  
 65 70 75 80  
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
 85 90 95  
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
 100 105 110  
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
 115 120 125  
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
 130 135 140  
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
 145 150 155 160  
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu  
 165 170 175  
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
 180 185 190  
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
 195 200 205  
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
 210 215 220  
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
 225 230 235 240

<210> 21  
 <211> 801  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(798)

<400> 21  
 atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg 48  
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala  
 1 5 10 15  
 gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg 96  
 Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg  
 20 25 30  
 gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc 144  
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu  
 35 40 45  
 gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt 192  
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val  
 50 55 60

cac agc ggg ccc gat gat ggc ccc tac gac gcc atg aac cgc ggc gtc	240
His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val	
65 70 75 80	
ggc gtg gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc	288
Gly Val Ala Thr Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr	
85 90 95	
ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac	336
Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp	
100 105 110	
cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg	384
His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr	
115 120 125	
aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag	432
Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu	
130 135 140	
acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac	480
Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp	
145 150 155 160	
ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac	528
Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp	
165 170 175	
ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg	576
Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met	
180 185 190	
gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg	624
Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg	
195 200 205	
cag ggg act gat aaa gag ttc aga aaa cgg ctg cca atg tac ttc tgg	672
Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp	
210 215 220	
gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac	720
Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp	
225 230 235 240	
aag gag aat cgc cgt ctg gcc ttg cgt acg cgg ttg ata agg gtt aag	768
Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys	
245 250 255	
gcc gtc tcc aaa gaa cga agc gca gaa ccg tag	801
Ala Val Ser Lys Glu Arg Ser Ala Glu Pro	
260 265	

&lt;210&gt; 22

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 22

Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
1 5 10 15

Val	Thr	Leu	Gln	Ala	Cys	Leu	Gly	Ser	Ile	Val	Gly	Gln	Thr	Tyr	Arg
			20					25					30		
Glu	Val	Glu	Val	Val	Leu	Val	Asp	Gly	Gly	Ser	Thr	Asp	Arg	Thr	Leu
		35					40					45			
Asp	Ile	Ala	Asn	Ser	Phe	Arg	Pro	Glu	Leu	Gly	Ser	Arg	Leu	Val	Val
	50					55					60				
His	Ser	Gly	Pro	Asp	Asp	Gly	Pro	Tyr	Asp	Ala	Met	Asn	Arg	Gly	Val
	65				70					75					80
Gly	Val	Ala	Thr	Gly	Glu	Trp	Val	Leu	Phe	Leu	Gly	Ala	Asp	Asp	Thr
				85					90					95	
Leu	Tyr	Glu	Pro	Thr	Thr	Leu	Ala	Gln	Val	Ala	Ala	Phe	Leu	Gly	Asp
			100					105					110		
His	Ala	Ala	Ser	His	Leu	Val	Tyr	Gly	Asp	Val	Val	Met	Arg	Ser	Thr
		115					120					125			
Lys	Ser	Arg	His	Ala	Gly	Pro	Phe	Asp	Leu	Asp	Arg	Leu	Leu	Phe	Glu
	130					135					140				
Thr	Asn	Leu	Cys	His	Gln	Ser	Ile	Phe	Tyr	Arg	Arg	Glu	Leu	Phe	Asp
	145				150					155					160
Gly	Ile	Gly	Pro	Tyr	Asn	Leu	Arg	Tyr	Arg	Val	Trp	Ala	Asp	Trp	Asp
				165					170					175	
Phe	Asn	Ile	Arg	Cys	Phe	Ser	Asn	Pro	Ala	Leu	Ile	Thr	Arg	Tyr	Met
			180					185					190		
Asp	Val	Val	Ile	Ser	Glu	Tyr	Asn	Asp	Met	Thr	Gly	Phe	Ser	Met	Arg
		195					200					205			
Gln	Gly	Thr	Asp	Lys	Glu	Phe	Arg	Lys	Arg	Leu	Pro	Met	Tyr	Phe	Trp
	210					215					220				
Val	Ala	Gly	Trp	Glu	Thr	Cys	Arg	Arg	Met	Leu	Ala	Phe	Leu	Lys	Asp
	225				230					235					240
Lys	Glu	Asn	Arg	Arg	Leu	Ala	Leu	Arg	Thr	Arg	Leu	Ile	Arg	Val	Lys
				245					250					255	
Ala	Val	Ser	Lys	Glu	Arg	Ser	Ala	Glu	Pro						
			260					265							

```
<210> 23
<211> 801
<212> DNA
<213> Mycobacterium
```

```
<220>  
<221> CDS  
<222> (1)..(798)
```

&lt;400&gt; 23

atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg	48
Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala	
1 5 10 15	
gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg	96
Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg	
20 25 30	
gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc	144
Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu	
35 40 45	
gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt	192
Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val	
50 55 60	
cac agc ggg ccc gat gat ggc ccc tac gac gcc atg aac cgc ggc gtc	240
His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val	
65 70 75 80	
ggc gta gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc	288
Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr	
85 90 95	
ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac	336
Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp	
100 105 110	
cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg	384
His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr	
115 120 125	
aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag	432
Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu	
130 135 140	
acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac	480
Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp	
145 150 155 160	
ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac	528
Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp	
165 170 175	
ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg	576
Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met	
180 185 190	
gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg	624
Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg	
195 200 205	
cag ggg act gat aaa gag ttc aga aaa cgg ctg cca atg tac ttc tgg	672
Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp	
210 215 220	
gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac	720
Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp	
225 230 235 240	

aag gag aat cgc cgt ctg gcc ttg cgt acg cgg ttg ata agg gtt aag 768  
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
                   245                  250                  255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801  
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
                   260                  265

<210> 24  
 <211> 266  
 <212> PRT  
 <213> Mycobacterium

<400> 24  
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala  
   1                  5                  10                  15  
 Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg  
                   20                  25                  30  
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu  
                   35                  40                  45  
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val  
                   50                  55                  60  
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val  
   65                  70                  75                  80  
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr  
                   85                  90                  95  
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp  
                   100                  105                  110  
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr  
                   115                  120                  125  
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu  
                   130                  135                  140  
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp  
   145                  150                  155                  160  
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp  
                   165                  170                  175  
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met  
                   180                  185                  190  
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg  
                   195                  200                  205  
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp  
                   210                  215                  220  
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp  
   225                  230                  235                  240



Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
245 250 255

Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
260 265

```
<210> 25
<211> 867
<212> DNA
<213> Mycobacterium
```

```
<220>  
<221> CDS  
<222> (1) .. (864)
```

<400> 25																
gtg	gcc	agc	aga	agt	ccc	cac	tcc	gct	gcg	ggt	ggt	tgg	cta	att	ctt	48
Val	Ala	Ser	Arg	Ser	Pro	His	Ser	Ala	Ala	Gly	Gly	Trp	Leu	Ile	Leu	
1				5				10				15				
ggc	ggc	tcc	ctt	ctt	gtg	gtc	ggc	gtg	gcg	cat	ccg	gta	gga	ctc	gcc	96
Gly	Gly	Ser	Leu	Leu	Val	Val	Gly	Val	Ala	His	Pro	Val	Gly	Leu	Ala	
20				25				30								
gga	ggt	gac	gac	gat	gct	ggc	gtg	gtg	cag	cag	ccg	atc	gag	gat	gct	144
Gly	Gly	Asp	Asp	Asp	Ala	Gly	Val	Val	Gln	Gln	Pro	Ile	Glu	Asp	Ala	
35				40				45								
ggc	ggc	ggt	ggt	gtg	ctc	ggg	cag	gaa	tcg	ccc	cca	ttg	ttc	gaa	ggg	192
Gly	Gly	Gly	Gly	Val	Leu	Gly	Gln	Glu	Ser	Pro	Pro	Leu	Phe	Glu	Gly	
50				55				60								
cca	atg	cga	ggc	gat	ggc	cag	gga	gcg	gcg	ctc	gta	gcc	ggc	agc	cac	240
Pro	Met	Arg	Gly	Asp	Gly	Gln	Gly	Ala	Ala	Leu	Val	Ala	Gly	Ser	His	
65				70				75				80				
gag	ccg	gaa	caa	cag	ttg	agt	ccc	ggt	gtc	gtc	gag	cgg	ggc	gaa	gcc	288
Glu	Pro	Glu	Gln	Gln	Leu	Ser	Pro	Gly	Val	Val	Glu	Arg	Gly	Glu	Ala	
85				90				95								
gat	ctc	gtc	caa	gat	gac	cag	atc	cgc	gcg	gag	cag	ggt	gtc	gat	gat	336
Asp	Leu	Val	Gln	Asp	Asp	Gln	Ile	Arg	Ala	Glu	Gln	Gly	Val	Asp	Asp	
100				105				110								
ctt	gcc	gac	ggt	gtt	gtc	ggc	cag	gcc	gcg	gta	gag	gac	ctc	gat	cag	384
Leu	Ala	Asp	Gly	Val	Val	Gly	Gln	Ala	Ala	Val	Glu	Asp	Leu	Asp	Gln	
115				120				125								
gtc	ggc	ggc	ggt	gaa	gta	gcg	gac	ttt	gaa	tcc	ggc	gtg	gac	ggc	agc	432
Val	Gly	Gly	Gly	Glu	Val	Ala	Asp	Phe	Glu	Ser	Gly	Val	Asp	Gly	Ser	
130				135				140								
gtg	ccc	gca	gcc	gat	gag	cag	gtg	act	ttt	gcc	cgt	acc	agg	tgg	gcc	480
Val	Pro	Ala	Ala	Asp	Glu	Gln	Val	Thr	Phe	Ala	Arg	Thr	Arg	Trp	Ala	
145				150				155				160				
aat	gac	cgc	cag	gtt	ctg	ttg	tgc	ccg	aat	cca	ttc	cag	gct	cga	cag	528
Asn	Asp	Arg	Gln	Val	Leu	Leu	Cys	Pro	Asn	Pro	Phe	Gln	Ala	Arg	Gln	
165				170				175								

gta gtc gaa cgt ggc tgc ggt gat cga cga tcc ggt gac gtc gaa ccc 576  
 Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro  
 180 185 190

gtc gag ggt ctt ggt gac cgg gaa ggc tgc ggc ctt gag acg gtt ggc 624  
 Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly  
 195 200 205

ggt gtt gga ggc atc gcg ggc agc gat ctc ggc ctc aac caa cgt ccg 672  
 Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro  
 210 215 220

cag gat ctc ctc cgg tgt cca gcg ttg cgt ctt ggc gac ttg caa cac 720  
 Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His  
 225 230 235 240

ctc ggc ggc gtt gcg gcg cac cgt ggc cag ctt caa ccg ccg cag cgc 768  
 Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg  
 245 250 255

cgc gtc aag gtc agc agc cag cgg tgc cgc cga gga cgg tgc cac cgg 816  
 Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg  
 260 265 270

ctt ggc agc ggt ggt cat gag gcc gtc ccg tcg gtg gtg ttg atc ttg 864  
 Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu  
 275 280 285

tag 867

<210> 26

<211> 288

<212> PRT

<213> Mycobacterium

<400> 26

Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu  
 1 5 10 15

Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala  
 20 25 30

Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala  
 35 40 45

Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly  
 50 55 60

Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His  
 65 70 75 80

Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala  
 85 90 95

Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp  
 100 105 110

Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln  
 115 120 125

Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser  
 130 135 140  
 Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala  
 145 150 155 160  
 Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln  
 165 170 175  
 Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro  
 180 185 190  
 Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly  
 195 200 205  
 Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro  
 210 215 220  
 Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His  
 225 230 235 240  
 Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg  
 245 250 255  
 Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg  
 260 265 270  
 Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu  
 275 280 285

&lt;210&gt; 27

&lt;211&gt; 1739

&lt;212&gt; DNA

&lt;213&gt; Mycobacterium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(945)

&lt;400&gt; 27

atg ggc tgc ctc aaa ggt ggt gtc gtc gcc aat gtt gtt gtt cca aca	48
Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr	
1 5 10 15	
ccg gat tat gtg cga ttc gcg tcc cac tat ggc ttc gtt ccg gac ttc	96
Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe	
20 25 30	
tgc cac ggt gcg gat ccg caa tcg aag ggc atc gtg gag aac ctc tgt	144
Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys	
35 40 45	
ggc tac gct cag gac gac ctt gcg gtg ccg ctg ctg acc gaa gct gcg	192
Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala	
50 55 60	
tta gcc ggt gag cag gtc gac cta cgt gcc ctc aac gcc cag gcg caa	240
Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln	
65 70 75 80	

cta tgg tgc gcc gag gtc aat gcc acg gtc cac tcg gag atc tgc gcc	288
Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala	
85 90 95	
gtg ccc aac gat cgc ttg gtt gac gag cgc acc gtc ttg agg gag ctg	336
Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu	
100 105 110	
ccc tcg ctg cgg ccg acg atc ggc tcg ggg tcg gtg cgc cgt aag gtc	384
Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val	
115 120 125	
gac ggc ctc tcg tgc atc cgt tac ggc tca gct cgt tac tcg gtg cct	432
Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro	
130 135 140	
cag cgg ctc gtc ggt gcc acc gtg gcg gtg gtg gtc gat cat ggc gcc	480
Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala	
145 150 155 160	
ctg atc ctg ttg gaa cct gcg acc ggt gtg atc gtg gcc gag cac gag	528
Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu	
165 170 175	
ctc gtc agc cca ggt gag gtg tcc atc ctc gat gaa cac tac gac gga	576
Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly	
180 185 190	
ccc aga ccc gca ccc tcg cgt ggt cct cgc ccg aaa acc caa gca gag	624
Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu	
195 200 205	
aaa cga ttc tgc gca ttg gga acc gaa gcg cag cag ttc ctc gtc ggt	672
Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly	
210 215 220	
gct gct gcg atc ggc aac acc cga ctg aaa tcc gaa ctc gac att ctg	720
Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu	
225 230 235 240	
ctc ggc ctt ggc gcc gcc cac ggc gaa cag gct ttg att gac gcg ctg	768
Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu	
245 250 255	
cgc cgg gcg gtt gcg ttt cgc cgg ttc cgc gct gcc gac gtg cgc tcg	816
Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser	
260 265 270	
atc ctg gcc gcc ggc gcc ggc acc cca caa ccc cgc ccc gcc ggc gac	864
Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp	
275 280 285	
gca ctc gtg ctc gat ctg ccc acc gtc gag acc cgc tcg ttg gag gcc	912
Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala	
290 295 300	
tac aag atc aac acc acc gac ggg acg gcc tca tgaccaccgc tgccaagccg	965
Tyr Lys Ile Asn Thr Asp Gly Thr Ala Ser	
305 310 315	
gtggcaccgt cctcggcggc accgctggct gctgaccttg acgcggcgct gcggcggttg	1025

aagctggcca cgggtgcgcc caacgccgcc gaggtgttgc aagtcgcca gacgcaacgc 1085  
tggacaccgg aggagatcct gcggacgttg gttgaggccg agatcgctgc ccgcatgcc 1145  
tccaacaccg ccaaccgtct caaggccgca gccttcccg tcaccaagac cctcgacggg 1205  
ttcgacgtca ccgcatcgtc gatcaccgca gccacgttcg actacctgtc gagcctggaa 1265  
tggattcggg cacaacagaa cctggcggtc attggccac ctggtacggg caaaagtcac 1325  
ctgctcatcg gctgcgggca cgctgccgtc cagccggat tcaaagtcg ctacttcacc 1385  
gccgccgacc tgatcgaggt cctctaccgc ggctggccg acaacaccgt cggcaagatc 1445  
atcgacaccc tgctccgctc ggatctggtc atcttgagc agatcggctt cggccgctc 1505  
gacgacaccg ggactcaact gttgttcgg ctctggctg ccggctacga gcgccgctcc 1565  
ctggccatcg cctcgcatcg gcccttcgaa caatgggggc gattcctgcc cgagcacacc 1625  
accgccgcca gcacctcga tcggctgctg caccacgcca gcacgtcgt cacctccggc 1685  
gagtcctacc ggatgcgcca cggcgaccac aagaaggag ccgccaagaa ttag 1739

<210> 28

<211> 315

<212> PRT

<213> Mycobacterium

<400> 28

Met	Gly	Cys	Leu	Lys	Gly	Gly	Val	Val	Ala	Asn	Val	Val	Val	Pro	Thr
1				5					10					15	
Pro	Asp	Tyr	Val	Arg	Phe	Ala	Ser	His	Tyr	Gly	Phe	Val	Pro	Asp	Phe
			20					25					30		
Cys	His	Gly	Ala	Asp	Pro	Gln	Ser	Lys	Gly	Ile	Val	Glu	Asn	Leu	Cys
		35					40					45			
Gly	Tyr	Ala	Gln	Asp	Asp	Leu	Ala	Val	Pro	Leu	Leu	Thr	Glu	Ala	Ala
	50					55					60				
Leu	Ala	Gly	Glu	Gln	Val	Asp	Leu	Arg	Ala	Leu	Asn	Ala	Gln	Ala	Gln
	65				70					75					80
Leu	Trp	Cys	Ala	Glu	Val	Asn	Ala	Thr	Val	His	Ser	Glu	Ile	Cys	Ala
				85					90					95	
Val	Pro	Asn	Asp	Arg	Leu	Val	Asp	Glu	Arg	Thr	Val	Leu	Arg	Glu	Leu
			100					105					110		
Pro	Ser	Leu	Arg	Pro	Thr	Ile	Gly	Ser	Gly	Ser	Val	Arg	Arg	Lys	Val
		115					120					125			
Asp	Gly	Leu	Ser	Cys	Ile	Arg	Tyr	Gly	Ser	Ala	Arg	Tyr	Ser	Val	Pro
	130					135					140				
Gln	Arg	Leu	Val	Gly	Ala	Thr	Val	Ala	Val	Val	Val	Asp	His	Gly	Ala
145					150					155					160

Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu  
 165 170 175  
 Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly  
 180 185 190  
 Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu  
 195 200 205  
 Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly  
 210 215 220  
 Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu  
 225 230 235 240  
 Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu  
 245 250 255  
 Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser  
 260 265 270  
 Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp  
 275 280 285  
 Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala  
 290 295 300  
 Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser  
 305 310 315

<210> 29

<211> 264

<212> PRT

<213> Mycobacterium

<220>

<221> DOMAIN

<222> (1)..(264)

<223> amino acid sequence is encoded by nucleotides  
945-1736 of SEQ ID NO:27

<400> 29

Met Thr Thr Ala Ala Lys Pro Val Ala Pro Ser Ser Ala Ala Pro Leu  
 1 5 10 15  
 Ala Ala Asp Leu Asp Ala Ala Leu Arg Arg Leu Lys Leu Ala Thr Val  
 20 25 30  
 Arg Arg Asn Ala Ala Glu Val Leu Gln Val Ala Lys Thr Gln Arg Trp  
 35 40 45  
 Thr Pro Glu Glu Ile Leu Arg Thr Leu Val Glu Ala Glu Ile Ala Ala  
 50 55 60  
 Arg Asp Ala Ser Asn Thr Ala Asn Arg Leu Lys Ala Ala Ala Phe Pro  
 65 70 75 80  
 Val Thr Lys Thr Leu Asp Gly Phe Asp Val Thr Gly Ser Ser Ile Thr  
 85 90 95

Ala Ala Thr Phe Asp Tyr Leu Ser Ser Leu Glu Trp Ile Arg Ala Gln  
 100 105 110

Gln Asn Leu Ala Val Ile Gly Pro Pro Gly Thr Gly Lys Ser His Leu  
 115 120 125

Leu Ile Gly Cys Gly His Ala Ala Val His Ala Gly Phe Lys Val Arg  
 130 135 140

Tyr Phe Thr Ala Ala Asp Leu Ile Glu Val Leu Tyr Arg Gly Leu Ala  
 145 150 155 160

Asp Asn Thr Val Gly Lys Ile Ile Asp Thr Leu Leu Arg Ala Asp Leu  
 165 170 175

Val Ile Leu Asp Glu Ile Gly Phe Ala Pro Leu Asp Asp Thr Gly Thr  
 180 185 190

Gln Leu Leu Phe Arg Leu Val Ala Ala Gly Tyr Glu Arg Arg Ser Leu  
 195 200 205

Ala Ile Ala Ser His Trp Pro Phe Glu Gln Trp Gly Arg Phe Leu Pro  
 210 215 220

Glu His Thr Thr Ala Ala Ser Ile Leu Asp Arg Leu Leu His His Ala  
 225 230 235 240

Ser Ile Val Val Thr Ser Gly Glu Ser Tyr Arg Met Arg His Ala Asp  
 245 250 255

His Lys Lys Gly Ala Ala Lys Asn  
 260

<210> 30  
 <211> 789  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(786)

<400> 30  
 gtg acg tct gct ccg acc gtc tcg gtg ata acg atc tcg ttc aac gac 48  
 Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp  
 1 5 10 15

ctc gac ggg ttg cag cgc acg gtg aaa agt gtg cgg gcg caa cgc tac 96  
 Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr  
 20 25 30

cgg gga cgc atc gag cac atc gta atc gac ggt ggc agc ggc gac gac 144  
 Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp  
 35 40 45

gtg gtg gca tac ctg tcc ggg tgt gaa cca ggc ttc gcg tat tgg cag 192  
 Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln  
 50 55 60

tcc gag ccc gac ggc ggg cgg tac gac gcg atg aac cag ggc atc gcg	240
Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala	
65 70 75 80	
cac gca tcg ggt gat ctg ttg tgg ttc ttg cac tcc gcc gat cgt ttt	288
His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe	
85 90 95	
tcc ggg ccc gac gtg gta gcc cag gcc gtg gag gcg cta tcc ggc aag	336
Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys	
100 105 110	
gga ccg gtg tcc gaa ttg tgg ggc ttc ggg atg gat cgt ctc gtc ggg	384
Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly	
115 120 125	
ctc gat cgg gtg cgc ggc ccg ata cct ttc agc ctg cgc aaa ttc ctg	432
Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu	
130 135 140	
gcc ggc aag cag gtt gtt ccg cat caa gca tcg ttc ttc gga tca tcg	480
Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser	
145 150 155 160	
ctg gtg gcc aag atc ggt ggc tac gac ctt gat ttc ggg atc gcc gcc	528
Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala	
165 170 175	
gac cag gaa ttc ata ttg cgg gcc gcg ctg gta tgc gag ccg gtc acg	576
Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr	
180 185 190	
att cgg tgt gtg ctg tgc gag ttc gac acc acg ggc gtc ggc tcg cac	624
Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His	
195 200 205	
cgg gaa cca agc gcg gtc ttc ggt gat ctg cgc cgc atg ggc gac ctt	672
Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu	
210 215 220	
cat cgc cgc tac ccg ttc ggg gga agg cga ata tca cat gcc tac cta	720
His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu	
225 230 235 240	
cgc ggc cgg gag ttc tac gcc tac aac agt cga ttc tgg gaa aac gtc	768
Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val	
245 250 255	
ttc acg cga atg tcg aaa tag	789
Phe Thr Arg Met Ser Lys	
260	

&lt;210&gt; 31

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 31

Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp
1 5 10 15



Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr  
                   20                                  25                                  30  
 Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp  
                   35                                  40                                  45  
 Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln  
                   50                                  55                                  60  
 Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala  
                   65                                  70                                  75                                  80  
 His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe  
                                   85                                  90                                  95  
 Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys  
                                   100                                  105                                  110  
 Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly  
                   115                                  120                                  125  
 Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu  
                   130                                  135                                  140  
 Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser  
                   145                                  150                                  155                                  160  
 Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala  
                                   165                                  170                                  175  
 Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr  
                                   180                                  185                                  190  
 Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His  
                   195                                  200                                  205  
 Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu  
                   210                                  215                                  220  
 His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu  
                   225                                  230                                  235                                  240  
 Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val  
                                   245                                  250                                  255  
 Phe Thr Arg Met Ser Lys  
                   260

<210> 32  
 <211> 1023  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1020)

&lt;400&gt; 32

gtg aag cga gcg ctc atc acc gga atc acc ggc cag gac ggc tcg tat	48
Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr	
1 5 10 15	
ctc gcc gaa ctg ctg ctg gcc aag ggg tat gag gtt cac ggg ctc atc	96
Leu Ala Glu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile	
20 25 30	
cgg cgc gct tcg acg ttc aac acc tcg cgg atc gat cac ctc tac gtc	144
Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val	
35 40 45	
gac ccg cac caa ccg ggc gcg cgg ctg ttt ctg cac tat ggt gac ctg	192
Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu	
50 55 60	
atc gac gga acc ccg ttg gtg acc ctg ctg agc acc atc gaa ccc gac	240
Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp	
65 70 75 80	
gag gtg tac aac ctg gcg gcg cag tca cac gtg cgg gtg agc ttc gac	288
Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp	
85 90 95	
gaa ccc gtg cac acc ggt gac acc acc ggc atg gga tcc atg cga ctg	336
Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu	
100 105 110	
ctg gaa gcc gtt ccg ctc tct ccg gtg cac tgc cgc ttc tat cag gcg	384
Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala	
115 120 125	
tcc tcg tcg gag atg ttc ggc gcc tcg ccg cca ccg cag aac gag ctg	432
Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu	
130 135 140	
acg ccg ttc tac ccg ccg tca ccg tat ggc gcc gcc aag gtc tat tcg	480
Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser	
145 150 155 160	
tac tgg gcg acc cgc aat tat cgc gaa gcg tac gga ttg ttc gcc gtt	528
Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val	
165 170 175	
aac ggc atc ttg ttc aat cac gaa tca ccg ccg cgc ggt gag acg ttc	576
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe	
180 185 190	
gtg acc cga aag atc acc agg gcc gtg gca cgc atc aag gcc ggt atc	624
Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile	
195 200 205	
cag tcc gag gtc tat atg ggc aat ctg gat gcg gtc cgc gac tgg ggg	672
Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly	
210 215 220	
tac gcg ccc gaa tac gtc gaa ggc atg tgg ccg atg ctg cag acc gac	720
Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp	
225 230 235 240	

gag ccc gac gac ttc gtt ttg gcg acc ggg cgc ggt ttc acc gtg cgt 768  
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg  
 245 250 255  
 gag ttc gcg cgg gcc gcg ttc gag cat gcc ggt ttg gac tgg cag cag 816  
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln  
 260 265 270  
 tac gtg aaa ttc gac caa cgc tat ctg cgg ccc acc gag gtg gat tcg 864  
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 ctg atc ggc gac gcg acc aag gct gcc gaa ttg ctg ggc tgg agg gct 912  
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala  
 290 295 300  
 tcg gtg cac act gac gag ttg gct cgg atc atg gtc gac gcg gac atg 960  
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met  
 305 310 315 320  
 gcg gcg ctg gag tgc gaa ggc aag ccg tgg atc gac aag ccg atg atc 1008  
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile  
 325 330 335  
 gcc ggc cgg aca tga 1023  
 Ala Gly Arg Thr  
 340

<210> 33  
 <211> 340  
 <212> PRT  
 <213> Mycobacterium

<400> 33  
 Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr  
 1 5 10 15  
 Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile  
 20 25 30  
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu  
 50 55 60  
 Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp  
 65 70 75 80  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu  
 100 105 110  
 Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu  
 130 135 140

Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser  
 145 150 155 160  
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp  
 225 230 235 240  
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg  
 245 250 255  
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln  
 260 265 270  
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala  
 290 295 300  
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met  
 305 310 315 320  
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile  
 325 330 335  
 Ala Gly Arg Thr  
 340

<210> 34  
 <211> 732  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(729)

<400> 34  
 atg agg ctg gcc cgt cgc gct cgg aac atc ttg cgt cgc aac ggc atc 48  
 Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile  
 1 5 10 15  
 gag gtg tcg cgc tac ttt gcc gaa ctg gac tgg gaa cgc aat ttc ttg 96  
 Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu  
 20 25 30

cgc caa ctg caa tcg cat cgg gtc agt gcc gtg ctc gat gtc ggg gcc	144
Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala	
35 40 45	
aat tcg ggg cag tac gcc agg ggt ctg cgc ggc gcg ggc ttc gcg ggc	192
Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly	
50 55 60	
cgc atc gtc tcg ttc gag ccg ctg ccc ggg ccc ttt gcc gtc ttg cag	240
Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln	
65 70 75 80	
cgc agc gcc tcc acg gac ccg ttg tgg gaa tgc cgg cgc tgt gcg ctg	288
Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu	
85 90 95	
ggc gat gtc gat gga acc atc tcg atc aac gtc gcc ggc aac gag ggc	336
Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly	
100 105 110	
gcc agc agt tcc gtc ttg ccg atg ttg aaa cga cat cag gac gcc ttt	384
Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe	
115 120 125	
cca cca gcc aac tac gtg ggc gcc caa cgg gtg ccg ata cat cga ctc	432
Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu	
130 135 140	
gat tcc gtg gct gca gac gtt ctg cgg ccc aac gat att gcg ttc ttg	480
Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu	
145 150 155 160	
aag atc gac gtt caa gga ttc gag aag cag gtg atc gcg ggt ggc gat	528
Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp	
165 170 175	
tca acg gtg cac gac cga tgc gtc ggc atg cag ctc gag ctg tct ttc	576
Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe	
180 185 190	
cag ccg ttg tac gag ggt ggc atg ctc atc cgc gag gcg ctc gat ctc	624
Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu	
195 200 205	
gtg gat tcg ttg ggc ttt acg ctc tcg gga ttg caa ccc ggt ttc acc	672
Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr	
210 215 220	
gac ccc cgc aac ggt cga atg ctg cag gcc gat ggc atc ttc ttc cgg	720
Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg	
225 230 235 240	
ggc agc gat tga	732
Gly Ser Asp	

&lt;210&gt; 35

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 35

Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile  
 1 5 10 15

Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu  
 20 25 30

Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala  
 35 40 45

Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly  
 50 55 60

Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln  
 65 70 75 80

Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu  
 85 90 95

Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly  
 100 105 110

Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe  
 115 120 125

Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu  
 130 135 140

Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu  
 145 150 155 160

Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp  
 165 170 175

Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe  
 180 185 190

Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu  
 195 200 205

Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr  
 210 215 220

Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg  
 225 230 235 240

Gly Ser Asp

&lt;210&gt; 36

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Mycobacterium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(729)

&lt;400&gt; 36

gtg	aaa	tcg	ttg	aaa	ctc	gct	cgt	ttc	atc	gcg	cgt	agc	gcc	gcc	ttc	48
Met	Lys	Ser	Leu	Lys	Leu	Ala	Arg	Phe	Ile	Ala	Arg	Ser	Ala	Ala	Phe	
1				5				10						15		
gag	gtt	tcg	cgc	cgc	tat	tct	gag	cga	gac	ctg	aag	cac	cag	ttt	gtg	96
Glu	Val	Ser	Arg	Arg	Tyr	Ser	Glu	Arg	Asp	Leu	Lys	His	Gln	Phe	Val	
			20					25					30			
aag	caa	ctc	aaa	tcg	cgt	cgg	gta	gat	gtc	gtt	ttc	gat	gtc	ggc	gcc	144
Lys	Gln	Leu	Lys	Ser	Arg	Arg	Val	Asp	Val	Val	Phe	Asp	Val	Gly	Ala	
		35					40					45				
aac	tca	gga	caa	tac	gcc	gcc	ggc	ctc	cgc	cga	gca	gca	tat	aag	ggc	192
Asn	Ser	Gly	Gln	Tyr	Ala	Ala	Gly	Leu	Arg	Arg	Ala	Ala	Tyr	Lys	Gly	
	50					55					60					
cgc	att	gtc	tcg	ttc	gaa	ccg	cta	tcc	gga	ccg	ttt	acg	atc	ttg	gaa	240
Arg	Ile	Val	Ser	Phe	Glu	Pro	Leu	Ser	Gly	Pro	Phe	Thr	Ile	Leu	Glu	
65					70				75					80		
agc	aaa	gcg	tca	acg	gat	cca	ctt	tgg	gat	tgc	cgg	cag	cat	gcg	ttg	288
Ser	Lys	Ala	Ser	Thr	Asp	Pro	Leu	Trp	Asp	Cys	Arg	Gln	His	Ala	Leu	
				85				90						95		
ggc	gat	tct	gat	gga	acg	gtt	acg	atc	aat	atc	gca	gga	aac	gcc	ggc	336
Gly	Asp	Ser	Asp	Gly	Thr	Val	Thr	Ile	Asn	Ile	Ala	Gly	Asn	Ala	Gly	
			100					105					110			
cag	agc	agt	tcc	gtc	ttg	ccc	atg	ctg	aaa	agt	cat	cag	aac	gct	ttt	384
Gln	Ser	Ser	Ser	Val	Leu	Pro	Met	Leu	Lys	Ser	His	Gln	Asn	Ala	Phe	
		115					120					125				
ccc	ccg	gca	aac	tat	gtc	ggc	acc	caa	gag	gca	tcc	ata	cat	cga	ctt	432
Pro	Pro	Ala	Asn	Tyr	Val	Gly	Thr	Gln	Glu	Ala	Ser	Ile	His	Arg	Leu	
	130					135					140					
gat	tcc	gtg	gca	cca	gaa	ttt	cta	ggc	atg	aac	ggc	gtc	gct	ttt	ctc	480
Asp	Ser	Val	Ala	Pro	Glu	Phe	Leu	Gly	Met	Asn	Gly	Val	Ala	Phe	Leu	
145				150					155					160		
aag	gtc	gac	gtt	caa	ggc	ttt	gaa	aag	cag	gtg	ctc	gcc	ggg	ggc	aaa	528
Lys	Val	Asp	Val	Gln	Gly	Phe	Glu	Lys	Gln	Val	Leu	Ala	Gly	Gly	Lys	
			165					170						175		
tca	acc	ata	gat	gac	cat	tgc	gtc	ggc	atg	caa	ctc	gaa	ctg	tcc	ttc	576
Ser	Thr	Ile	Asp	Asp	His	Cys	Val	Gly	Met	Gln	Leu	Glu	Leu	Ser	Phe	
			180					185					190			
ctg	ccg	ttg	tac	gaa	ggc	ggc	atg	ctc	att	cct	gaa	gcc	ctc	gat	ctc	624
Leu	Pro	Leu	Tyr	Glu	Gly	Gly	Met	Leu	Ile	Pro	Glu	Ala	Leu	Asp	Leu	
		195					200					205				
gtg	tat	tcc	ttg	ggc	ttc	acg	ttg	acg	gga	ttg	ctg	cct	tgt	ttc	att	672
Val	Tyr	Ser	Leu	Gly	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Pro	Cys	Phe	Ile	
	210					215					220					
gat	gca	aat	aat	ggc	cga	atg	ttg	cag	gcc	gac	ggc	atc	ttt	ttc	cgc	720
Asp	Ala	Asn	Asn	Gly	Arg	Met	Leu	Gln	Ala	Asp	Gly	Ile	Phe	Phe	Arg	
225					230					235					240	

gag gac gat tga  
Glu Asp Asp

<210> 37  
<211> 243  
<212> PRT  
<213> Mycobacterium

<400> 37  
Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe  
1 5 10 15  
Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val  
20 25 30  
Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala  
35 40 45  
Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly  
50 55 60  
Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu  
65 70 75 80  
Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu  
85 90 95  
Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly  
100 105 110  
Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe  
115 120 125  
Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu  
130 135 140  
Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu  
145 150 155 160  
Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys  
165 170 175  
Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe  
180 185 190  
Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu  
195 200 205  
Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile  
210 215 220  
Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg  
225 230 235 240  
Glu Asp Asp

<210> 38  
<211> 828



&lt;212&gt; DNA

&lt;213&gt; Mycobacterium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(825)

&lt;400&gt; 38

atg gtg cag acg aaa cga tac gcc ggc ttg acc gca gct aac aca aag	48
Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys	
1 5 10 15	
aaa gtc gcc atg gcc gca cca atg ttt tgc atc atc atc ccc acc ttg	96
Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu	
20 25 30	
aac gtg gct gcg gta ttg cct gcc tgc ctc gac agc atc gcc cgt cag	144
Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln	
35 40 45	
acc tgc ggt gac ttc gag ctg gta ctg gtc gac ggc ggc tgc acg gac	192
Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp	
50 55 60	
gaa acc ctc gac atc gcc aac att ttc gcc ccc aac ctc ggc gag cgg	240
Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg	
65 70 75 80	
ttg atc att cat cgc gac acc gac cag ggc gtc tac gac gcc atg aac	288
Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn	
85 90 95	
cgc ggc gtg gac ctg gcc acc gga acg tgg ttg ctc ttt ctg ggc gcg	336
Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala	
100 105 110	
gac gac agc ctg tac gag gct gac acc ctg gcg cgg gtg gcc gcc ttc	384
Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe	
115 120 125	
att ggc gaa cac gag ccc agc gat ctg gta tat ggc gac gtg atc atg	432
Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met	
130 135 140	
cgc tca acc aat ttc cgc tgg ggt ggc gcc ttc gac ctc gac cgt ctg	480
Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu	
145 150 155 160	
ttg ttc aag cgc aac atc tgc cat cag gcg atc ttc tac cgc cgc gga	528
Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly	
165 170 175	
ctc ttc ggc acc atc ggt ccc tac aac ctc cgc tac cgg gtc ctg gcc	576
Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala	
180 185 190	
gac tgg gac ttc aat att cgc tgc ttt tcc aac cca gcg ctc gtc acc	624
Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr	
195 200 205	

cgc tac atg cac gtg gtc gtt gca agc tac aac gaa ttc ggc ggg ctc	672
Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu	
210 215 220	
agc aat acg atc gtc gac aag gag ttt ttg aag cgg ctg ccg atg tcc	720
Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser	
225 230 235 240	
acg aga ctc ggc ata agg ctg gtc ata gtt ctg gtg cgc agg tgg cca	768
Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro	
245 250 255	
aag gtg atc agc agg gcc atg gta atg cgc acc gtc att tct tgg cgg	816
Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg	
260 265 270	
cgc cga cgt tag	828
Arg Arg Arg	
275	

<210> 39  
 <211> 275  
 <212> PRT  
 <213> Mycobacterium

<400> 39	
Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys	
1 5 10 15	
Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu	
20 25 30	
Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln	
35 40 45	
Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp	
50 55 60	
Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg	
65 70 75 80	
Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn	
85 90 95	
Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala	
100 105 110	
Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe	
115 120 125	
Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met	
130 135 140	
Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu	
145 150 155 160	
Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly	
165 170 175	

Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala  
 180 185 190  
 Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr  
 195 200 205  
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu  
 210 215 220  
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser  
 225 230 235 240  
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro  
 245 250 255  
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg  
 260 265 270  
 Arg Arg Arg  
 275

<210> 40  
 <211> 24  
 <212> DNA  
 <213> Mycobacterium

<400> 40  
 gatgccgtga ggaggtaaag ctgc

24

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Mycobacterium

<400> 41  
 gatacggctc ttgaatcctg cacg

24